

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/223,263DATE: 07/01/94  
TIME: 13:29:35

INPUT SET: S8190.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Eaton, Dan L.  
DeSauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

(iii) NUMBER OF SEQUENCES: 32

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: patin (Genentech)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263  
(B) FILING DATE: 4-APR-1994  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689  
(B) FILING DATE: 15-FEB-1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607  
(B) FILING DATE: 21-JAN-1994

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553  
(B) FILING DATE: 3-JAN-1994

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.  
(B) REGISTRATION NUMBER: 32,637  
(C) REFERENCE/DOCKET NUMBER: 871P3

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47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: 415/225-1249
50 (B) TELEFAX: 415/952-9881
51 (C) TELEX: 910/371-7168
52
53 (2) INFORMATION FOR SEQ ID NO:1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 353 amino acids
57 (B) TYPE: amino acid
58 (D) TOPOLOGY: linear
59
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
63 1 5 10 15
64
65 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
66 20 25 30
67
68 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
69 35 40 45
70
71 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
72 50 55 60
73
74 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
75 65 70 75
76
77 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
78 80 85 90
79
80 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
81 95 100 105
82
83 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
84 110 115 120
85
86 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
87 125 130 135
88
89 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
90 140 145 150
91
92 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
93 155 160 165
94
95 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
96 170 175 180
97
98 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
99 185 190 195

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100
101   Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
102                               200                               205                               210
103
104   Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
105                               215                               220                               225
106
107   Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
108                               230                               235                               240
109
110   Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
111                               245                               250                               255
112
113   Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
114                               260                               265                               270
115
116   Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
117                               275                               280                               285
118
119   Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
120                               290                               295                               300
121
122   Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
123                               305                               310                               315
124
125   Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
126                               320                               325                               330
127
128   Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
129                               335                               340                               345
130
131   Ser Gln Asn Leu Ser Gln Glu Gly
132                               350                               353
133

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

143
144
145   TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
146
147
148   CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
149
150
151   CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
152

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153  
154 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200  
155  
156  
157 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250  
158  
159  
160 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTG TG 300  
161  
162  
163 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350  
164  
165  
166 AGACTGAGCC AGTGCCCAAG GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400  
167  
168  
169 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450  
170  
171  
172 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500  
173  
174  
175 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550  
176  
177  
178 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600  
179  
180  
181 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650  
182  
183  
184 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700  
185  
186  
187 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750  
188  
189  
190 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800  
191  
192  
193 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850  
194  
195  
196 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900  
197  
198  
199 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950  
200  
201  
202 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACCTCGT GACTCTTTCC 1000  
203  
204  
205 TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050

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206  
207  
208 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100  
209  
210  
211 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150  
212  
213  
214 CTTGCCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200  
215  
216  
217 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250  
218  
219  
220 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300  
221  
222  
223 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350  
224  
225  
226 AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400  
227  
228  
229 GGGATACACA GGACTGAAAA GGGAATCATT TTTCCTGTA CATTATAAAC 1450  
230  
231  
232 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500  
233  
234  
235 GCTCTTTGGT CTATTTTCTG CAGAAATTG CAACTCACTG ATTCTCTACA 1550  
236  
237  
238 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600  
239  
240  
241 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650  
242  
243  
244 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700  
245  
246  
247 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750  
248  
249  
250 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795  
251  
252  
253

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/223,263**

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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/223263